



SEQUENCE LISTING

#10/a

TO610

- (1) GENERAL INFORMATION
- (i) APPLICANT: BOIME, Irving  
MOYLE, William R.
  - (ii) TITLE OF THE INVENTION: SINGLE-CHAIN FORMS OF THE  
GLYCOPROTEIN HORMONE QUARTET
  - (iii) NUMBER OF SEQUENCES: 83
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: MORRISON & FOERSTER
    - (B) STREET: 2000 Pennsylvania Avenue, NW, suite 5500
    - (C) CITY: Washington
    - (D) STATE: DC
    - (E) COUNTRY: USA
    - (F) ZIP: 20006-1888
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Diskette
    - (B) COMPUTER: IBM Compatible
    - (C) OPERATING SYSTEM: DOS
    - (D) SOFTWARE: FastSEQ for Windows Version 2.0
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/918,288
    - (B) FILING DATE: 25 AUG-1997
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/853,524
    - (B) FILING DATE: 09-MAY-1997
    - (A) APPLICATION NUMBER: 08/199,382
    - (B) FILING DATE: 18-FEB-1994
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Murashige, Kate H
    - (B) REGISTRATION NUMBER: 29,959
    - (C) REFERENCE/DOCKET NUMBER: 29500-20050.25
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 202-887-1500
    - (B) TELEFAX: 202-887-0763
    - (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 amino acids
    - (B) TYPE: amino acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ser | Ser | Lys | Ala | Pro | Pro | Pro | Ser | Leu | Pro | Ser | Pro | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Pro | Gly | Pro | Ser | Asp | Thr | Pro | Ile | Leu | Pro | Gln |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 836 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 33...827  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|   |            |            |    |     |     |     |     |     |     |     |    |
|---|------------|------------|----|-----|-----|-----|-----|-----|-----|-----|----|
| ATGAAATCGA  | CGGAATCAGA | CTCGAGCCAA | GG | ATG | GAG | ATG | TTC | CAG | GGG | CTG | 53 |
|   |            |            |    | Met | Glu | Met | Phe | Gln | Gly | Leu |    |
|   |            |            |    | 1   |     |     |     | 5   |     |     |    |
| CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG | 101        |            |    |     |     |     |     |     |     |     |    |
| Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu |            |            |    |     |     |     |     |     |     |     |    |
| 10 15 20  |            |            |    |     |     |     |     |     |     |     |    |
| CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG | 149        |            |    |     |     |     |     |     |     |     |    |
| Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu |            |            |    |     |     |     |     |     |     |     |    |
| 25 30 35  |            |            |    |     |     |     |     |     |     |     |    |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 197        |            |    |     |     |     |     |     |     |     |    |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala |            |            |    |     |     |     |     |     |     |     |    |
| 40 45 50 55   |            |            |    |     |     |     |     |     |     |     |    |
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC | 245        |            |    |     |     |     |     |     |     |     |    |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala |            |            |    |     |     |     |     |     |     |     |    |
| 60 65 70  |            |            |    |     |     |     |     |     |     |     |    |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC | 293        |            |    |     |     |     |     |     |     |     |    |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile |            |            |    |     |     |     |     |     |     |     |    |
| 75 80 85  |            |            |    |     |     |     |     |     |     |     |    |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC | 341        |            |    |     |     |     |     |     |     |     |    |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala |            |            |    |     |     |     |     |     |     |     |    |
| 90 95 100   |            |            |    |     |     |     |     |     |     |     |    |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC | 389        |            |    |     |     |     |     |     |     |     |    |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp |            |            |    |     |     |     |     |     |     |     |    |

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| 105   | 110 | 115 |     |
|---|-----|-----|-----|
| TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC |     |     | 437 |
| Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe |     |     |     |
| 120   | 125 | 130 | 135 |
| CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA |     |     | 485 |
| Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro |     |     |     |
|   | 140 | 145 | 150 |
| TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC |     |     | 533 |
| Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser |     |     |     |
|   | 155 | 160 | 165 |
| GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA TGC |     |     | 581 |
| Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys |     |     |     |
|   | 170 | 175 | 180 |
| ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA CTT |     |     | 629 |
| Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu |     |     |     |
|   | 185 | 190 | 195 |
| CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA AGG |     |     | 677 |
| Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg |     |     |     |
| 200   | 205 | 210 | 215 |
| TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC ACT |     |     | 725 |
| Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr |     |     |     |
|   | 220 | 225 | 230 |
| TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT TTC |     |     | 773 |
| Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe |     |     |     |
|   | 235 | 240 | 245 |
| AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT CAC |     |     | 821 |
| Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His |     |     |     |
|   | 250 | 255 | 260 |
| AAA TCT TAAGGTACC   |     |     | 836 |
| Lys Ser   |     |     |     |
| 265   |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile |     |     |     |
|   | 20  | 25  | 30  |
| Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr |     |     |     |
|   | 35  | 40  | 45  |
| Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val |     |     |     |
|   | 50  | 55  | 60  |
| Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg |     |     |     |
|   | 65  | 70  | 75  |
| Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val |     |     |     |
|   | 85  | 90  | 95  |
| Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu |     |     |     |
|   | 100 | 105 | 110 |
| Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu |     |     |     |
|   | 115 | 120 | 125 |
| Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro |     |     |     |
|   | 130 | 135 | 140 |
| Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr |     |     |     |
|   | 145 | 150 | 155 |
| Pro Ile Leu Pro Gln Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp |     |     |     |
|   | 165 | 170 | 175 |
| Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser |     |     |     |
|   | 180 | 185 | 190 |
| Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg |     |     |     |
|   | 195 | 200 | 205 |
| Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys |     |     |     |
|   | 210 | 215 | 220 |
| Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg |     |     |     |
|   | 225 | 230 | 235 |
| Val Thr Val Met Gly Phe Lys Val Glu Asn His Thr Ala Cys His     |     |     |     |
|   | 245 | 250 | 255 |
| Cys Ser Thr Cys Tyr Tyr His Lys Ser                             |     |     |     |
|   | 260 | 265 |     |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TCCGGATTAG | CTTGAGATGG | ATCCGGTACC | TTAAGATTTG | TGATAATAAC | AAGTACTGCA | 60  |
| GTGGCACGCC | GTGTGGTTCT | CCACTTTGAA | ACCCCCATT  | ACTGTGACCC | TGTTATATGA | 120 |
| TTTAGCTACA | CAGCAAGTGG | ACTCTGAGGT | GACGTTCTTT | TGGACCAACA | TCGTCTTCTT | 180 |
| GGACCTTAGT | GGAGTGGGAT | ATGCTCTAGA | GAAGCAGCAG | CCCATGCACT | GAAGTATTGG | 240 |
| GGCACCCGGC | TGGGAGAAGA | ATGGGTTTTT | CTGTAGCGTG | CATTCTGGGC | AATCCTGCAC | 300 |
| ATCAGGAGCG | CTACCAGATC | CGCTACCGGA | TCCTTGGGGG | AGGATCGGGG | TGTCCGAGGG | 360 |
| CCCCGGGAGT | CGGGATGGGC | TTGGAAGGCT | GGGGGGAGGG | GCCTTTGAGG | AAGAGGAGTC | 420 |
| CTGGAAGCGG | GGGTCATCAC | AGGTCAAGGG | GTGGTCCTTG | GGACCCCCGC | AGTCAGTGGT | 480 |
| GCTGCGGCGG | CAGAGTGCAC | ATTGACAGCT | GAGAGCCACG | GCGTAGGAGA | CCACGGGGTT | 540 |
| CACGCCGCGC | GGGCAGCCAG | GGAGCCGGAT | GGACTCGAAG | CGCACATCGC | GGTAGTTGCA | 600 |
| CACCACCTGA | GGCAGGGCCG | GCAGGACCCC | CTGCAGCACG | CGGGTCATGG | TGGGGCAGTA | 660 |
| GCCGGCACAG | ATGGTGGTGT | TGACGGTGAT | GCACACGGGG | CAGCCCTCCT | TCTCCACAGC | 720 |

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CAGGGTGGCA TTGATGGGGC GGCACCGTGG CCGAAGCGGC TCCTTGGATG CCCATGTCCC 780  
 GCCCATGCTC AGCAGCAGCA ACAGCAGCAG CCCCTGGAAC ATCTCCATCC TTGG 834

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|   |     |
|---|-----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG GAG ATG TTC CAG GGG CTG | 53  |
| Met Glu Met Phe Gln Gly Leu                                     |     |
| 1 5   |     |
| CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG | 101 |
| Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu |     |
| 10 15 20  |     |
| CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG | 149 |
| Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu |     |
| 25 30 35  |     |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 197 |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala |     |
| 40 45 50 55   |     |
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC | 245 |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala |     |
| 60 65 70  |     |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC | 293 |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile |     |
| 75 80 85  |     |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC | 341 |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala |     |
| 90 95 100   |     |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC | 389 |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Ser Thr Thr Asp     |     |
| 105 110 115   |     |
| TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCG CGG GGA | 437 |
| Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Gly |     |
| 120 125 130 135   |     |
| TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA | 485 |
| Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu |     |

|   |     |     |
|---|-----|-----|
| 130   | 135 | 140 |
| Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe |     |     |
| 145   | 150 | 155 |
| Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser |     | 160 |
|   | 165 | 170 |
| Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln |     | 175 |
|   | 180 | 185 |
| Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn |     | 190 |
|   | 195 | 200 |
| Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys |     | 205 |
|   | 210 | 215 |
| His Cys Ser Thr Cys Tyr Tyr His Lys Ser                         |     | 220 |
| 225   | 230 |     |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|   |     |
|---|-----|
| GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC | 60  |
| TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGACTC | 120 |
| TGAGGTGACG TTCTTTTGGG CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC | 180 |
| TCTAGAGAAG CAGCAGCCCA TGCCTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG  | 240 |
| GTTTTCTGT AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT  | 300 |
| ACCGGATCCC CGCGGGTCAT CACAGGTCAA GGGGTGGTCC TTGGGACCCC CGCAGTCAGT | 360 |
| GGTGCTGCGG CGGCAGAGTG CACATTGACA GCTGAGAGCC ACGGCGTAGG AGACCACGGG | 420 |
| GTTACGCGCG CGCGGGCAGC CAGGGAGCCG GATGGACTCG AAGCGCACAT CGCGGTAGTT | 480 |
| GCACACCACC TGAGGCAGGG CCGGCAGGAC CCCCTGCAGC ACGCGGGTCA TGGTGGGGCA | 540 |
| GTAGCCGGCA CAGATGGTGG TGTGACGGT GATGCACACG GGGCAGCCCT CCTTCTCCAC  | 600 |
| AGCCAGGGTG GCATTGATGG GCGGCACCG TGGCCGAAGC GGCTCCTTGG ATGCCCATGT  | 660 |
| CCCGCCCATG CTCAGCAGCA GCAACAGCAG CAGCCCCTGG AACATCTCCA TCCTTGG    | 717 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...735
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|  |    |
|--|----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGA ATG GAG ATG CTC CAG GGG CTG | 54 |
| Met Glu Met Leu Gln Gly Leu                                      |    |
| 1 5  |    |

| 140 |     |     |           |     |     |     |     |     |     | 145 |     |     |     |     | 150 |     |  |  |  |  |
|-----|-----|-----|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| TGC | ACG | CTA | CAG       | GAA | AAC | CCA | TTC | TTC | TCC | CAG | CCG | GGT | GCC | CCA | ATA | 533 |  |  |  |  |
| Cys | Thr | Leu | Gln       | Glu | Asn | Pro | Phe | Phe | Ser | Gln | Pro | Gly | Ala | Pro | Ile |     |  |  |  |  |
|     |     |     | 155       |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |  |  |  |  |
| CTT | CAG | TGC | ATG       | GGC | TGC | TGC | TTC | TCT | AGA | GCA | TAT | CCC | ACT | CCA | CTA | 581 |  |  |  |  |
| Leu | Gln | Cys | Met       | Gly | Cys | Cys | Phe | Ser | Arg | Ala | Tyr | Pro | Thr | Pro | Leu |     |  |  |  |  |
|     |     | 170 |           |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     |  |  |  |  |
| AGG | TCC | AAG | AAG       | ACG | ATG | TTG | GTC | CAA | AAG | AAC | GTC | ACC | TCA | GAG | TCC | 629 |  |  |  |  |
| Arg | Ser | Lys | Lys       | Thr | Met | Leu | Val | Gln | Lys | Asn | Val | Thr | Ser | Glu | Ser |     |  |  |  |  |
|     | 185 |     |           |     |     | 190 |     |     |     |     | 195 |     |     |     |     |     |  |  |  |  |
| ACT | TGC | TGT | GTA       | GCT | AAA | TCA | TAT | AAC | AGG | GTC | ACA | GTA | ATG | GGG | GGT | 677 |  |  |  |  |
| Thr | Cys | Cys | Val       | Ala | Lys | Ser | Tyr | Asn | Arg | Val | Thr | Val | Met | Gly | Gly |     |  |  |  |  |
| 200 |     |     |           |     | 205 |     |     |     |     | 210 |     |     |     | 215 |     |     |  |  |  |  |
| TTC | AAA | GTG | GAG       | AAC | CAC | ACG | GCG | TGC | CAC | TGC | AGT | ACT | TGT | TAT | TAT | 725 |  |  |  |  |
| Phe | Lys | Val | Glu       | Asn | His | Thr | Ala | Cys | His | Cys | Ser | Thr | Cys | Tyr | Tyr |     |  |  |  |  |
|     |     |     | 220       |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |  |  |  |  |
| CAC | AAA | TCT | TAAGGTACC |     |     |     |     |     |     |     |     |     |     |     |     | 743 |  |  |  |  |
| His | Lys | Ser |           |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Phe | Gln | Gly | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Met | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Thr | Trp | Ala | Ser | Lys | Glu | Pro | Leu | Arg | Pro | Arg | Cys | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     | Ile |
| Asn | Ala | Thr | Leu | Ala | Val | Glu | Lys | Gly | Cys | Pro | Val | Cys | Ile | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asn | Thr | Thr | Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     | Val |
| Leu | Gln | Gly | Val | Leu | Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Val | Arg | Phe | Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | Val |
| Asn | Pro | Val | Val | Ser | Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     | Leu |
| Cys | Arg | Arg | Ser | Thr | Thr | Asp | Cys | Gly | Gly | Pro | Lys | Asp | His | Pro |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     | Leu |
| Thr | Cys | Asp | Asp | Pro | Arg | Gly | Ser | Gly | Ser | Gly | Ser | Gly | Ser | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | Pro |

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|   |     |
|---|-----|
| CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG GCA TGG GCA TCC AGG GAG | 102 |
| Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Ala Trp Ala Ser Arg Glu |     |
| 10 15 20  |     |
| CCG CTT CGG CCA TGG TGC CAC CCC ATC AAT GCC ATC CTG GCT GTG GAG | 150 |
| Pro Leu Arg Pro Trp Cys His Pro Ile Asn Ala Ile Leu Ala Val Glu |     |
| 25 30 35  |     |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 198 |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala |     |
| 40 45 50 55   |     |
| GGC TAC TGC CCC ACC ATG ATG CGC GTG CTG CAG GCG GTC CTG CCG CCC | 246 |
| Gly Tyr Cys Pro Thr Met Met Arg Val Leu Gln Ala Val Leu Pro Pro |     |
| 60 65 70  |     |
| CTG CCT CAG GTG GTG TGC ACC TAC CGT GAT GTG CGC TTC GAG TCC ATC | 294 |
| Leu Pro Gln Val Val Cys Thr Tyr Arg Asp Val Arg Phe Glu Ser Ile |     |
| 75 80 85  |     |
| CGG CTC CCT GGC TGC CCG CGT GGC GTG GAC CCC GTG GTC TCC TTC CCT | 342 |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asp Pro Val Val Ser Phe Pro |     |
| 90 95 100   |     |
| GTG GCT CTC AGC TGT CGC TGT GGA CCC TGC CGC CGC AGC ACC TCT GAC | 390 |
| Val Ala Leu Ser Cys Arg Cys Gly Pro Cys Arg Arg Ser Thr Ser Asp |     |
| 105 110 115   |     |
| TGT GGG GGT CCC AAA GAC CAC CCC TTG ACC TGT GAC CAC CCC CAA GGA | 438 |
| Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp His Pro Gln Gly |     |
| 120 125 130 135   |     |
| TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA | 486 |
| Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu |     |
| 140 145 150   |     |
| TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA | 534 |
| Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile |     |
| 155 160 165   |     |
| CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA | 582 |
| Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu |     |
| 170 175 180   |     |
| AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC | 630 |
| Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser |     |
| 185 190 195   |     |
| ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT | 678 |
| Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly |     |
| 200 205 210 215   |     |
| TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT | 726 |
| Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr |     |
| 220 225 230   |     |

68

CAC AAA TCT TAAGGTACC  
His Lys Ser

744

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Leu | Gln | Gly | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Met | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Ala | Trp | Ala | Ser | Arg | Glu | Pro | Leu | Arg | Pro | Trp | Cys | His | Pro | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Ile | Leu | Ala | Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asn | Thr | Thr | Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Met | Arg | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gln | Ala | Val | Leu | Pro | Leu | Pro | Gln | Val | Val | Cys | Thr | Tyr | Arg |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Arg | Phe | Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Pro | Val | Val | Ser | Phe | Pro | Val | Ala | Leu | Ser | Cys | Arg | Cys | Gly | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Arg | Arg | Ser | Thr | Ser | Asp | Cys | Gly | Gly | Pro | Lys | Asp | His | Pro | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Cys | Asp | His | Pro | Gln | Gly | Ser | Gly | Ser | Gly | Ser | Gly | Ser | Ala | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Val | Gln | Asp | Cys | Pro | Glu | Cys | Thr | Leu | Gln | Glu | Asn | Pro | Phe | Phe |
| 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu | Gln | Cys | Met | Gly | Cys | Cys | Phe | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg | Ser | Lys | Lys | Thr | Met | Leu | Val | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr | Cys | Cys | Val | Ala | Lys | Ser | Tyr | Asn |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Val | Thr | Val | Met | Gly | Gly | Phe | Lys | Val | Glu | Asn | His | Thr | Ala | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Cys | Ser | Thr | Cys | Tyr | His | Lys | Ser |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|   |     |
|---|-----|
| GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC | 60  |
| TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGACTC | 120 |
| TGAGGTGACG TTCTTTTGGG CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC | 180 |
| TCTAGAGAAG CAGCAGCCCA TGCACTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG | 240 |
| GTTTTCTGT AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT  | 300 |
| ACCGGATCCT TGGGGGTGGT CACAGGTCAA GGGGTGGTCT TTGGGACCCC CACAGTCAGA | 360 |
| GGTGCTGCGG CGGCAGGGTC CACAGCGACA GCTGAGAGCC ACAGGGAAGG AGACCACGGG | 420 |
| GTCCACGCCA CGCGGGCAGC CAGGGAGCCG GATGGACTCG AAGCGCACAT CACGGTAGGT | 480 |
| GCACACCACC TGAGGCAGGG GCGGCAGGAC CGCCTGCAGC ACGCGCATCA TGGTGGGGCA | 540 |
| GTAGCCGGCA CAGATGGTGG TGTTGACGGT GATGCACACG GGGCAGCCCT CCTTCTCCAC | 600 |
| AGCCAGGATG GCATTGATGG GGTGGCACCA TGGCCGAAGC GGCTCCCTGG ATGCCCATGC | 660 |
| CCCGCCCATG CTCAGCAGCA GCAACAGCAG CAGCCCCTGG AGCATCTCCA TTCCTTGG   | 718 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...719
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|   |     |
|---|-----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG AAG ACA CTC CAG TTT TTC | 53  |
| Met Lys Thr Leu Gln Phe Phe                                     |     |
| 1 5   |     |
| TTC CTT TTC TGT TGC TGG AAA GCA ATC TGC TGC AAT AGC TGT GAG CTG | 101 |
| Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys Asn Ser Cys Glu Leu |     |
| 10 15 20  |     |
| ACC AAC ATC ACC ATT GCA ATA GAG AAA GAA GAA TGT CGT TTC TGC ATA | 149 |
| Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe Cys Ile |     |
| 25 30 35  |     |
| AGC ATC AAC ACC ACT TGG TGT GCT GGC TAC TGC TAC ACC AGG GAT CTG | 197 |
| Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu |     |
| 40 45 50 55   |     |
| GTG TAT AAG GAC CCA GCC AGG CCC AAA ATC CAG AAA ACA TGT ACC TTC | 245 |
| Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe |     |
| 60 65 70  |     |
| AAG GAA CTG GTA TAT GAA ACA GTG AGA GTG CCC GGC TGT GCT CAC CAT | 293 |
| Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His |     |
| 75 80 85  |     |
| GCA GAT TCC TTG TAT ACA TAC CCA GTG GCC ACC CAG TGT CAC TGT GGC | 341 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |           |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------|-----|-----|--|
| Ala | Asp | Ser | Leu | Tyr | Thr | Tyr | Pro | Val | Ala | Thr | Gln | Cys | His | Cys       | Gly |     |  |
|     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |           |     |     |  |
| AAG | TGT | GAC | AGC | GAC | AGC | ACT | GAT | TGT | ACT | GTG | CGA | GGC | CTG | GGG       | CCC | 389 |  |
| Lys | Cys | Asp | Ser | Asp | Ser | Thr | Asp | Cys | Thr | Val | Arg | Gly | Leu | Gly       | Pro |     |  |
|     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |     |           |     |     |  |
| AGC | TAC | TGC | TCC | TTT | GGT | GAA | ATG | AAA | GAA | GGA | TCC | GGT | AGC | GGA       | TCT | 437 |  |
| Ser | Tyr | Cys | Ser | Phe | Gly | Glu | Met | Lys | Glu | Gly | Ser | Gly | Ser | Gly       | Ser |     |  |
|     | 120 |     |     |     | 125 |     |     |     |     | 130 |     |     |     |           | 135 |     |  |
| GGT | AGC | GCT | CCT | GAT | GTG | CAG | GAT | TGC | CCA | GAA | TGC | ACG | CTA | CAG       | GAA | 485 |  |
| Gly | Ser | Ala | Pro | Asp | Val | Gln | Asp | Cys | Pro | Glu | Cys | Thr | Leu | Gln       | Glu |     |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150       |     |     |  |
| AAC | CCA | TTC | TTC | TCC | CAG | CCG | GGT | GCC | CCA | ATA | CTT | CAG | TGC | ATG       | GGC | 533 |  |
| Asn | Pro | Phe | Phe | Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu | Gln | Cys | Met       | Gly |     |  |
|     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |           |     |     |  |
| TGC | TGC | TTC | TCT | AGA | GCA | TAT | CCC | ACT | CCA | CTA | AGG | TCC | AAG | AAG       | ACG | 581 |  |
| Cys | Cys | Phe | Ser | Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg | Ser | Lys | Lys       | Thr |     |  |
|     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |     |           |     |     |  |
| ATG | TTG | GTC | CAA | AAG | AAC | GTC | ACC | TCA | GAG | TCC | ACT | TGC | TGT | GTA       | GCT | 629 |  |
| Met | Leu | Val | Gln | Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr | Cys | Cys | Val       | Ala |     |  |
|     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |           |     |     |  |
| AAA | TCA | TAT | AAC | AGG | GTC | ACA | GTA | ATG | GGG | GGT | TTC | AAA | GTG | GAG       | AAC | 677 |  |
| Lys | Ser | Tyr | Asn | Arg | Val | Thr | Val | Met | Gly | Gly | Phe | Lys | Val | Glu       | Asn |     |  |
|     | 200 |     |     |     | 205 |     |     |     | 210 |     |     |     |     | 215       |     |     |  |
| CAC | ACG | GCG | TGC | CAC | TGC | AGT | ACT | TGT | TAT | TAT | CAC | AAA | TCT | TAAGGTACC | 728 |     |  |
| His | Thr | Ala | Cys | His | Cys | Ser | Thr | Cys | Tyr | Tyr | His | Lys | Ser |           |     |     |  |
|     |     |     | 220 |     |     |     |     |     | 225 |     |     |     |     |           |     |     |  |

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Lys | Thr | Leu | Gln | Phe | Phe | Phe | Leu | Phe | Cys | Cys | Trp | Lys | Ala | Ile |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Cys | Cys | Asn | Ser | Cys | Glu | Leu | Thr | Asn | Ile | Thr | Ile | Ala | Ile | Glu | Lys |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Glu | Glu | Cys | Arg | Phe | Cys | Ile | Ser | Ile | Asn | Thr | Thr | Trp | Cys | Ala | Gly |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Tyr | Cys | Tyr | Thr | Arg | Asp | Leu | Val | Tyr | Lys | Asp | Pro | Ala | Arg | Pro | Lys |  |  |

|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |
| Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg |     |     |     |     |
| 65  |     | 70  |     | 75  |
| Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val |     |     |     | 80  |
|   | 85  |     | 90  | 95  |
| Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys |     |     |     |     |
|   | 100 |     | 105 | 110 |
| Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys |     |     |     |     |
|   | 115 |     | 120 | 125 |
| Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys |     |     |     |     |
|   | 130 |     | 135 | 140 |
| Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala |     |     |     |     |
| 145   |     | 150 |     | 155 |
| Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr |     |     |     |     |
|   | 165 |     | 170 | 175 |
| Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser |     |     |     |     |
|   | 180 |     | 185 | 190 |
| Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met |     |     |     |     |
|   | 195 |     | 200 | 205 |
| Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys |     |     |     |     |
|   | 210 |     | 215 | 220 |
| Tyr Tyr His Lys Ser   |     |     |     |     |
| 225   |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|  |     |
|--|-----|
| GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCCTCCAC | 60  |
| TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGACTC  | 120 |
| TGAGGTGACG TTCTTTTGGG CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC  | 180 |
| TCTAGAGAAG CAGCAGCCCA TGCCTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG   | 240 |
| GTTTTCTCTGT AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT | 300 |
| ACCGGATCCT TCTTTTCATT CACCAAAGGA GCAGTAGCTG GGCCCCAGGC CTCGCACAGT  | 360 |
| ACAATCAGTG CTGTCGCTGT CACACTTGCC ACAGTGACAC TGGGTGGCCA CTGGGTATGT  | 420 |
| ATACAAGGAA TCTGCATGGT GAGCACAGCC GGGCACTCTC ACTGTTTCAT ATACCAAGTTC | 480 |
| CTTGAAGGTA CATGTTTTCT GGATTTTGGG CCTGGCTGGG TCCTTATACA CCAGATCCCT  | 540 |
| GGTGTAGCAG TAGCCAGCAC ACCAAGTGGT GTTGATGCTT ATGCAGAAAC GACATTCTTC  | 600 |
| TTTCTCTATT GCAATGGTGA TGTGGTCAG CTCACAGCTA TTGCAGCAGA TTGCTTTCCA   | 660 |
| GCAACAGAAA AGGAAGAAAA ACTGGAGTGT CTTTCATCCTT GG                    | 702 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

72

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 33...743  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|   |                             |    |
|---|-----------------------------|----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG                             | ATG GAG ATG TTC CAG GGG CTG | 53 |
|   | Met Glu Met Phe Gln Gly Leu |    |
|   | 1 5                         |    |
| CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG | 101                         |    |
| Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu |                             |    |
|   | 10 15 20                    |    |
| CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG | 149                         |    |
| Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu |                             |    |
|   | 25 30 35                    |    |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 197                         |    |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala |                             |    |
|   | 40 45 50 55                 |    |
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC | 245                         |    |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala |                             |    |
|   | 60 65 70                    |    |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC | 293                         |    |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile |                             |    |
|   | 75 80 85                    |    |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC | 341                         |    |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala |                             |    |
|   | 90 95 100                   |    |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC GAC AGC GAC AGC ACT GAT | 389                         |    |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Asp Ser Asp Ser Thr Asp |                             |    |
|   | 105 110 115                 |    |
| TGT ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC TCC TTT GGT GAA ATG | 437                         |    |
| Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met |                             |    |
|   | 120 125 130 135             |    |
| AAA GAA GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT | 485                         |    |
| Lys Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp |                             |    |
|   | 140 145 150                 |    |
| TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT | 533                         |    |
| Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly |                             |    |
|   | 155 160 165                 |    |
| GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC | 581                         |    |
| Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro |                             |    |
|   | 170 175 180                 |    |
| ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC | 629                         |    |
| Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr |                             |    |

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|   |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|
| 185   |     | 190 |     | 195 |     |
| TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA |     |     |     |     | 677 |
| Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val |     |     |     |     |     |
| 200   |     | 205 |     | 210 | 215 |
| ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT |     |     |     |     | 725 |
| Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr |     |     |     |     |     |
|   | 220 |     | 225 |     | 230 |
| TGT TAT TAT CAC AAA TCT TAAGGTACC                               |     |     |     |     | 752 |
| Cys Tyr Tyr His Lys Ser   |     |     |     |     |     |
|   | 235 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Phe | Gln | Gly | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Met | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Thr | Trp | Ala | Ser | Lys | Glu | Pro | Leu | Arg | Pro | Arg | Cys | Arg | Pro | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Thr | Leu | Ala | Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asn | Thr | Thr | Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gln | Gly | Val | Leu | Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Arg | Phe | Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Pro | Val | Val | Ser | Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Asp | Ser | Asp | Ser | Thr | Asp | Cys | Thr | Val | Arg | Gly | Leu | Gly | Pro | Ser |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Tyr | Cys | Ser | Phe | Gly | Glu | Met | Lys | Glu | Gly | Ser | Gly | Ser | Gly | Ser | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ala | Pro | Asp | Val | Gln | Asp | Cys | Pro | Glu | Cys | Thr | Leu | Gln | Glu | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Phe | Phe | Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu | Gln | Cys | Met | Gly | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Phe | Ser | Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg | Ser | Lys | Lys | Thr | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Val | Gln | Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr | Cys | Cys | Val | Ala | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Tyr | Asn | Arg | Val | Thr | Val | Met | Gly | Gly | Phe | Lys | Val | Glu | Asn | His |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Ala | Cys | His | Cys | Ser | Thr | Cys | Tyr | Tyr | His | Lys | Ser |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GGTACCTTAA GATTTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC      60
TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTTA GCTACACAGC AAGTGGGACTC     120
TGAGGTGACG TTCTTTTGGG CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC     180
TCTAGAGAAG CAGCAGCCCA TGCAGTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG     240
GTTTTCTGTG AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT     300
ACCGGATCCT TCTTTTCATT CACCAAAGGA GCAGTAGCTG GGCCCCAGGC CTCGCACAGT     360
ACAATCAGTG CTGTCGCTGT CGCAGAGTGC ACATTGACAG CTGAGAGCCA CGGCGTAGGA     420
GACCACGGGG TTCACGCCGC GCGGGCAGCC AGGGAGCCGG ATGGACTCGA AGCGCACATC     480
GCGGTAGTTG CACACCACCT GAGGCAGGGC CGGCAGGACC CCCTGCAGCA CGCGGGTCAT     540
GGTGGGGCAG TAGCCGGCAC AGATGGTGGT GTTGACGGTG ATGCACACGG GGCAGCCCTC     600
CTTCTCCACA GCCAGGGTGG CATTGATGGG GCGGCACCGT GGCCGAAGCG GCTCCTTGGA     660
TGCCCATGTC CCGCCCATGC TCAGCAGCAG CAACAGCAGC AGCCCCTGGA ACATCTCCAT     720
CCTTGG                                     726

```

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...743
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG GAG ATG TTC CAG GGG CTG      53
                               Met Glu Met Phe Gln Gly Leu
                               1             5

CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG      101
Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu
    10             15             20

CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG      149
Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu
    25             30             35

AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC      197
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala

```

| 40  | 45  | 50  | 55  |     |
|---|-----|-----|-----|-----|
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC |     |     |     | 245 |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala | 60  | 65  | 70  |     |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC |     |     |     | 293 |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile | 75  | 80  | 85  |     |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC |     |     |     | 341 |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala | 90  | 95  | 100 |     |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC |     |     |     | 389 |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp | 105 | 110 | 115 |     |
| TGC ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC TCC TTT GGT GAA ATG |     |     |     | 437 |
| Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met | 120 | 125 | 130 | 135 |
| AAA GAA GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT |     |     |     | 485 |
| Lys Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp | 140 | 145 | 150 |     |
| TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT |     |     |     | 533 |
| Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly | 155 | 160 | 165 |     |
| GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC |     |     |     | 581 |
| Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro | 170 | 175 | 180 |     |
| ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC |     |     |     | 629 |
| Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr | 185 | 190 | 195 |     |
| TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA |     |     |     | 677 |
| Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val | 200 | 205 | 210 | 215 |
| ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT |     |     |     | 725 |
| Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr | 220 | 225 | 230 |     |
| TGT TAT TAT CAC AAA TCT TAAGGTACC                               |     |     |     | 752 |
| Cys Tyr Tyr His Lys Ser   | 235 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 237 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Phe | Gln | Gly | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Met | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Thr | Trp | Ala | Ser | Lys | Glu | Pro | Leu | Arg | Pro | Arg | Cys | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     | Ile |
| Asn | Ala | Thr | Leu | Ala | Val | Glu | Lys | Gly | Cys | Pro | Val | Cys | Ile | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Val | Asn | Thr | Thr | Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     | Val |
| Leu | Gln | Gly | Val | Leu | Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Val | Arg | Phe | Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | Val |
| Asn | Pro | Val | Val | Ser | Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     | Leu |
| Cys | Arg | Arg | Ser | Thr | Thr | Asp | Cys | Thr | Val | Arg | Gly | Leu | Gly | Pro |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     | Ser |
| Tyr | Cys | Ser | Phe | Gly | Glu | Met | Lys | Glu | Gly | Ser | Gly | Ser | Gly | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     | Gly |
| Ser | Ala | Pro | Asp | Val | Gln | Asp | Cys | Pro | Glu | Cys | Thr | Leu | Gln | Glu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | Asn |
| Pro | Phe | Phe | Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu | Gln | Cys | Met | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | Cys |
| Cys | Phe | Ser | Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg | Ser | Lys | Lys | Thr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     | Met |
| Leu | Val | Gln | Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr | Cys | Cys | Val | Ala |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     | Lys |
| Ser | Tyr | Asn | Arg | Val | Thr | Val | Met | Gly | Gly | Phe | Lys | Val | Glu | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     | His |
| Thr | Ala | Cys | His | Cys | Ser | Thr | Cys | Tyr | Tyr | His | Lys | Ser |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTACCTTAA | GATTTGTGAT | AATAACAAGT | ACTGCAGTGG | CACGCCGTGT | GGTTCTCCAC | 60  |
| TTTGAAACCC | CCCATTACTG | TGACCCTGTT | ATATGATTTA | GCTACACAGC | AAGTGGACTC | 120 |
| TGAGGTGACG | TTCTTTTGGA | CCAACATCGT | CTTCTTGGAC | CTTAGTGGAG | TGGGATATGC | 180 |
| TCTAGAGAAG | CAGCAGCCCA | TGCACTGAAG | TATTGGGGCA | CCCGGCTGGG | AGAAGAATGG | 240 |
| GTTTTCTGT  | AGCGTGCATT | CTGGGCAATC | CTGCACATCA | GGAGCGCTAC | CAGATCCGCT | 300 |
| ACCGGATCCT | TCTTTTATTT | CACCAAAGGA | GCAGTAGCTG | GGCCCCAGGC | CTCGCACAGT | 360 |
| GCAGTCAGTG | GTGCTGCGGC | GGCAGAGTGC | ACATTGACAG | CTGAGAGCCA | CGGCGTAGGA | 420 |
| GACCACGGGG | TTCACGCCGC | GCGGGCAGCC | AGGGAGCCGG | ATGGACTCGA | AGCGCACATC | 480 |

|   |     |
|---|-----|
| CGGGTAGTTG CACACCACCT GAGGCAGGGC CGGCAGGACC CCCTGCAGCA CGCGGGTCAT | 540 |
| GGTGGGGCAG TAGCCGGCAC AGATGGTGGT GTTGACGGTG ATGCACACGG GGCAGCCCTC | 600 |
| CTTCTCCACA GCCAGGGTGG CATTGATGGG GCGGCACCGT GGCCGAAGCG GCTCCTTGGA | 660 |
| TGCCCATGTC CCGCCCATGC TCAGCAGCAG CAACAGCAGC AGCCCTGGA ACATCTCCAT  | 720 |
| CCTTGG  | 726 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|   |                             |    |
|---|-----------------------------|----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG                             | ATG GAG ATG TTC CAG GGG CTG | 53 |
|   | Met Glu Met Phe Gln Gly Leu |    |
|   | 1 5                         |    |
| CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG | 101                         |    |
| Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu     |                             |    |
| 10 15 20  |                             |    |
| CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG | 149                         |    |
| Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu |                             |    |
| 25 30 35  |                             |    |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 197                         |    |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala |                             |    |
| 40 45 50 55   |                             |    |
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC | 245                         |    |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala |                             |    |
| 60 65 70  |                             |    |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC | 293                         |    |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile |                             |    |
| 75 80 85  |                             |    |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC | 341                         |    |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala |                             |    |
| 90 95 100   |                             |    |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC | 389                         |    |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp |                             |    |
| 105 110 115   |                             |    |
| TGC ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC TCC TTT GGT GAA GGA | 437                         |    |
| Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Gly |                             |    |
| 120 125 130 135   |                             |    |

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|   |     |
|---|-----|
| TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA | 485 |
| Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu |     |
| 140 145 150   |     |
| TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA | 533 |
| Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile |     |
| 155 160 165   |     |
| CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA | 581 |
| Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu |     |
| 170 175 180   |     |
| AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC | 629 |
| Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser |     |
| 185 190 195   |     |
| ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT | 677 |
| Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly |     |
| 200 205 210 215   |     |
| TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT | 725 |
| Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr |     |
| 220 225 230   |     |
| CAC AAA TCT TAAGGTACC   | 743 |
| His Lys Ser   |     |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|   |  |
|---|--|
| Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly     |  |
| 1 5 10 15   |  |
| Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile |  |
| 20 25 30  |  |
| Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr |  |
| 35 40 45  |  |
| Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val |  |
| 50 55 60  |  |
| Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg |  |
| 65 70 75 80   |  |
| Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val |  |
| 85 90 95  |  |
| Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu |  |
| 100 105 110   |  |

Cys Arg Arg Ser Thr Thr Asp Cys Thr Val Arg Gly Leu Gly Pro Ser  
 115 120 125  
 Tyr Cys Ser Phe Gly Glu Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro  
 130 135 140  
 Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe  
 145 150 155 160  
 Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser  
 165 170 175  
 Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln  
 180 185 190  
 Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn  
 195 200 205  
 Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys  
 210 215 220  
 His Cys Ser Thr Cys Tyr Tyr His Lys Ser  
 225 230

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTACCTTAA | GATTTGTGAT | AATAACAAGT | ACTGCAGTGG | CACGCCGTGT | GGTTCTCCAC | 60  |
| TTTGAAACCC | CCCATTACTG | TGACCCTGTT | ATATGATTTA | GCTACACAGC | AAGTGGACTC | 120 |
| TGAGGTGACG | TTCTTTTGGA | CCAACATCGT | CTTCTTGGAC | CTTAGTGGAG | TGGGATATGC | 180 |
| TCTAGAGAAG | CAGCAGCCCA | TGCACTGAAG | TATTGGGGCA | CCCGGCTGGG | AGAAGAATGG | 240 |
| GTTTTCTGT  | AGCGTGCATT | CTGGGCAATC | CTGCACATCA | GGAGCGCTAC | CAGATCCGCT | 300 |
| ACCGGATCCT | TCACCAAAGG | AGCAGTAGCT | GGGCCCCAGG | CCTCGCACAG | TGCAGTCAGT | 360 |
| GGTGCTGCGG | CGGCAGAGTG | CACATTGACA | GCTGAGAGCC | ACGGCGTAGG | AGACCACGGG | 420 |
| GTTCACGCCG | CGCGGGCAGC | CAGGGAGCCG | GATGGACTCG | AAGCGCACAT | CGCGGTAGTT | 480 |
| GCACACCACC | TGAGGCAGGG | CCGGCAGGAC | CCCCTGCAGC | ACGCGGGTCA | TGGTGGGGCA | 540 |
| GTAGCCGGCA | CAGATGGTGG | TGTTGACGGT | GATGCACACG | GGGCAGCCCT | CCTTCTCCAC | 600 |
| AGCCAGGGTG | GCATTGATGG | GGCGGCACCG | TGGCCGAAGC | GGCTCCTTGG | ATGCCCATGT | 660 |
| CCCGCCCATG | CTCAGCAGCA | GCAACAGCAG | CAGCCCCTGG | AACATCTCCA | TCCTTGG    | 717 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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|   |                             |    |
|---|-----------------------------|----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG                             | ATG GAG ATG TTC CAG GGG CTG | 53 |
|   | Met Glu Met Phe Gln Gly Leu |    |
|   | 1 5                         |    |
| CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG | 101                         |    |
| Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu |                             |    |
| 10 15 20  |                             |    |
| CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG | 149                         |    |
| Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu |                             |    |
| 25 30 35  |                             |    |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 197                         |    |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala |                             |    |
| 40 45 50 55   |                             |    |
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC | 245                         |    |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala |                             |    |
| 60 65 70  |                             |    |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC | 293                         |    |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile |                             |    |
| 75 80 85  |                             |    |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC | 341                         |    |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala |                             |    |
| 90 95 100   |                             |    |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC | 389                         |    |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp |                             |    |
| 105 110 115   |                             |    |
| TGC ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC GAT GAC CCG CGG GGA | 437                         |    |
| Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Asp Asp Pro Arg Gly |                             |    |
| 120 125 130 135   |                             |    |
| TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA | 485                         |    |
| Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu |                             |    |
| 140 145 150   |                             |    |
| TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA | 533                         |    |
| Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile |                             |    |
| 155 160 165   |                             |    |
| CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA | 581                         |    |
| Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu |                             |    |
| 170 175 180   |                             |    |
| AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC | 629                         |    |
| Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser |                             |    |
| 185 190 195   |                             |    |
| ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT | 677                         |    |
| Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly |                             |    |
| 200 205 210 215   |                             |    |
| TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT | 725                         |    |



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTACCTTAA | GATTTGTGAT | AATAACAAGT | ACTGCAGTGG | CACGCCGTGT | GGTTCTCCAC | 60  |
| TTTGAAACCC | CCCATTACTG | TGACCCTGTT | ATATGATTTA | GCTACACAGC | AAGTGGACTC | 120 |
| TGAGGTGACG | TTCTTTTGGG | CCAACATCGT | CTTCTTGGAC | CTTAGTGGAG | TGGGATATGC | 180 |
| TCTAGAGAAG | CAGCAGCCCC | TGCACTGAAG | TATTGGGGCA | CCCGGCTGGG | AGAAGAATGG | 240 |
| GTTTTCTGT  | AGCGTGCATT | CTGGGCAATC | CTGCACATCA | GGAGCGCTAC | CAGATCCGCT | 300 |
| ACCGGATCCC | CGCGGGTCAT | CGCAGTAGCT | GGGCCCCAGG | CCTCGCACAG | TGCAGTCAGT | 360 |
| GGTGCTGCGG | CGGCAGAGTG | CACATTGACA | GCTGAGAGCC | ACGGCGTAGG | AGACCACGGG | 420 |
| GTTACAGCCG | CGCGGGCAGC | CAGGGAGCCG | GATGGACTCG | AAGCGCACAT | CGCGGTAGTT | 480 |
| GCACACCACC | TGAGGCAGGG | CCGGCAGGAC | CCCCTGCAGC | ACGCGGGTCA | TGGTGGGGCA | 540 |
| GTAGCCGGCA | CAGATGGTGG | TGTTGACGGT | GATGCACACG | GGGCAGCCCT | CCTTCTCCAC | 600 |
| AGCCAGGGTG | GCATTGATGG | GGCGGCACCG | TGGCCGAAGC | GGCTCCTTGG | ATGCCCATGT | 660 |
| CCCGCCCATG | CTCAGCAGCA | GCAACAGCAG | CAGCCCCTGG | AACATCTCCA | TCCTTGG    | 717 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 33...700  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|            |            |            |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATGAAATCGA | CGGAATCAGA | CTCGAGCCAA | GG  | ATG | AAG | ACA | CTC | CAG | TTT | TTC | 53  |
|            |            |            | Met | Lys | Thr | Leu | Gln | Phe | Phe |     |     |
|            |            |            | 1   |     |     |     | 5   |     |     |     |     |
| TTC        | CTT        | TTC        | TGT | TGC | TGG | AAA | GCA | ATC | TGC | TGC | 101 |
| Phe        | Leu        | Phe        | Cys | Cys | Trp | Lys | Ala | Ile | Cys | Cys |     |
|            | 10         |            |     |     |     | 15  |     |     | 20  |     |     |
| ACC        | AAC        | ATC        | ACC | ATT | GCA | ATA | GAG | AAA | GAA | GAA | 149 |
| Thr        | Asn        | Ile        | Thr | Ile | Ala | Ile | Glu | Lys | Glu | Glu |     |
|            | 25         |            |     |     | 30  |     |     |     | 35  |     |     |
| AGC        | ATC        | AAC        | ACC | ACT | TGG | TGT | GCT | GGC | TAC | TGC | 197 |
| Ser        | Ile        | Asn        | Thr | Thr | Trp | Cys | Ala | Gly | Tyr | Cys |     |
|            | 40         |            |     |     | 45  |     |     | 50  |     |     |     |
| GTG        | TAT        | AAG        | GAC | CCA | GCC | AGG | CCC | AAA | ATC | CAG | 245 |
| Val        | Tyr        | Lys        | Asp | Pro | Ala | Arg | Pro | Lys | Ile | Gln |     |
|            |            |            | 60  |     |     |     |     | 65  |     |     |     |
| AAG        | GAA        | CTG        | GTA | TAT | GAA | ACA | GTG | AGA | GTG | CCC | 293 |
| Lys        | Glu        | Leu        | Val | Tyr | Glu | Thr | Val | Arg | Val | Pro |     |
|            |            |            |     |     |     |     |     |     |     |     |     |

| 75  |     |     |     |     |     |     |     |            |           | 80  |     |     |     |     | 85  |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|------------|-----------|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| GCA | GAT | TCC | TTG | TAT | ACA | TAC | CCA | GTG        | GCC       | ACC | CAG | TGT | CAC | TGT | GGC | 341 |  |  |  |  |
| Ala | Asp | Ser | Leu | Tyr | Thr | Tyr | Pro | Val        | Ala       | Thr | Gln | Cys | His | Cys | Gly |     |  |  |  |  |
| 90  |     |     |     |     |     | 95  |     |            |           |     |     | 100 |     |     |     |     |  |  |  |  |
| AAG | TGT | GAC | AGC | GAC | AGC | ACT | GAT | TGT        | ACT       | GTG | CGA | GGC | CTG | GGG | CCC | 389 |  |  |  |  |
| Lys | Cys | Asp | Ser | Asp | Ser | Thr | Asp | Cys        | Thr       | Val | Arg | Gly | Leu | Gly | Pro |     |  |  |  |  |
| 105 |     |     |     |     |     | 110 |     |            |           |     |     | 115 |     |     |     |     |  |  |  |  |
| AGC | TAC | TGC | TCC | TTT | GGT | GAA | GGA | TCC        | GGT       | AGC | GGA | TCT | GGT | AGC | GCT | 437 |  |  |  |  |
| Ser | Tyr | Cys | Ser | Phe | Gly | Glu | Gly | Ser        | Gly       | Ser | Gly | Ser | Gly | Ser | Ala |     |  |  |  |  |
| 120 |     |     | 125 |     |     |     |     |            | 130       |     |     | 135 |     |     |     |     |  |  |  |  |
| CCT | GAT | GTG | CAG | GAT | TGC | CCA | GAA | TGC        | ACG       | CTA | CAG | GAA | AAC | CCA | TTC | 485 |  |  |  |  |
| Pro | Asp | Val | Gln | Asp | Cys | Pro | Glu | Cys        | Thr       | Leu | Gln | Glu | Asn | Pro | Phe |     |  |  |  |  |
|     |     |     | 140 |     |     |     |     |            | 145       |     |     | 150 |     |     |     |     |  |  |  |  |
| TTC | TCC | CAG | CCG | GGT | GCC | CCA | ATA | CTT        | CAG       | TGC | ATG | GGC | TGC | TGC | TTC | 533 |  |  |  |  |
| Phe | Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu        | Gln       | Cys | Met | Gly | Cys | Cys | Phe |     |  |  |  |  |
| 155 |     |     |     |     |     | 160 |     |            |           |     |     | 165 |     |     |     |     |  |  |  |  |
| TCT | AGA | GCA | TAT | CCC | ACT | CCA | CTA | AGG        | TCC       | AAG | AAG | ACG | ATG | TTG | GTC | 581 |  |  |  |  |
| Ser | Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg        | Ser       | Lys | Lys | Thr | Met | Leu | Val |     |  |  |  |  |
| 170 |     |     |     |     |     | 175 |     |            |           |     |     | 180 |     |     |     |     |  |  |  |  |
| CAA | AAG | AAC | GTC | ACC | TCA | GAG | TCC | ACT        | TGC       | TGT | GTA | GCT | AAA | TCA | TAT | 629 |  |  |  |  |
| Gln | Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr        | Cys       | Cys | Val | Ala | Lys | Ser | Tyr |     |  |  |  |  |
| 185 |     |     |     |     |     | 190 |     |            |           |     |     | 195 |     |     |     |     |  |  |  |  |
| AAC | AGG | GTC | ACA | GTA | ATG | GGG | GGT | TTC        | AAA       | GTG | GAG | AAC | CAC | ACG | GCG | 677 |  |  |  |  |
| Asn | Arg | Val | Thr | Val | Met | Gly | Gly | Phe        | Lys       | Val | Glu | Asn | His | Thr | Ala |     |  |  |  |  |
| 200 |     |     | 205 |     |     |     |     |            | 210       |     |     | 215 |     |     |     |     |  |  |  |  |
| TGC | CAC | TGC | AGT | ACT | TGT | TAT | TA  | TCACAAATCT | TAAGGTACC |     |     |     |     |     |     | 719 |  |  |  |  |
| Cys | His | Cys | Ser | Thr | Cys | Tyr | Tyr |            |           |     |     |     |     |     |     |     |  |  |  |  |
|     |     |     | 220 |     |     |     |     |            |           |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Leu | Gln | Phe | Phe | Phe | Leu | Phe | Cys | Cys | Trp | Lys | Ala | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Cys | Asn | Ser | Cys | Glu | Leu | Thr | Asn | Ile | Thr | Ile | Ala | Ile | Glu | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Cys | Arg | Phe | Cys | Ile | Ser | Ile | Asn | Thr | Thr | Trp | Cys | Ala | Gly |

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(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 33...698  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|   |     |
|---|-----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG AAG ACA CTC CAG TTT TTC | 53  |
| Met Lys Thr Leu Gln Phe Phe                                     |     |
| 1 5   |     |
| TTC CTT TTC TGT TGC TGG AAA GCA ATC TGC TGC AAT AGC TGT GAG CTG | 101 |
| Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys Asn Ser Cys Glu Leu |     |
| 10 15 20  |     |
| ACC AAC ATC ACC ATT GCA ATA GAG AAA GAA GAA TGT CGT TTC TGC ATA | 149 |
| Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe Cys Ile |     |
| 25 30 35  |     |
| AGC ATC AAC ACC ACT TGG TGT GCT GGC TAC TGC TAC ACC AGG GAT CTG | 197 |
| Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu |     |
| 40 45 50 55   |     |
| GTG TAT AAG GAC CCA GCC AGG CCC AAA ATC CAG AAA ACA TGT ACC TTC | 245 |
| Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe |     |
| 60 65 70  |     |
| AAG GAA CTG GTA TAT GAA ACA GTG AGA GTG CCC GGC TGT GCT CAC CAT | 293 |
| Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His |     |
| 75 80 85  |     |
| GCA GAT TCC TTG TAT ACA TAC CCA GTG GCC ACC CAG TGT CAC TGT GGC | 341 |
| Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr Gln Cys His Cys Gly |     |
| 90 95 100   |     |
| AAG TGT GAC AGC GAC AGC ACT GAT TGT ACT GTG CGA GGC CTG GGG CCC | 389 |
| Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val Arg Gly Leu Gly Pro |     |
| 105 110 115   |     |
| AGC TAC TGC GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG | 437 |
| Ser Tyr Cys Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln |     |
| 120 125 130 135   |     |
| GAT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG | 485 |
| Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro |     |
| 140 145 150   |     |
| GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT | 533 |
| Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr |     |
| 155 160 165   |     |
| CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC | 581 |
| Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val |     |
| 170 175 180   |     |
| ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA | 629 |
| Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr |     |

820

|   |  |     |  |     |     |
|---|--|-----|--|-----|-----|
| 185   |  | 190 |  | 195 |     |
| GTA ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT |  |     |  |     | 677 |
| Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser |  |     |  |     |     |
| 200   |  | 205 |  | 210 | 215 |
| ACT TGT TAT TAT CAC AAA TCT TAAGGTACC                           |  |     |  |     | 707 |
| Thr Cys Tyr Tyr His Lys Ser                                     |  |     |  |     |     |
| 220   |  |     |  |     |     |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Leu | Gln | Phe | Phe | Phe | Leu | Phe | Cys | Cys | Trp | Lys | Ala | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Cys | Cys | Asn | Ser | Cys | Glu | Leu | Thr | Asn | Ile | Thr | Ile | Ala | Ile | Glu | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Glu | Cys | Arg | Phe | Cys | Ile | Ser | Ile | Asn | Thr | Thr | Trp | Cys | Ala | Gly |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Cys | Tyr | Thr | Arg | Asp | Leu | Val | Tyr | Lys | Asp | Pro | Ala | Arg | Pro | Lys |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ile | Gln | Lys | Thr | Cys | Thr | Phe | Lys | Glu | Leu | Val | Tyr | Glu | Thr | Val | Arg |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Val | Pro | Gly | Cys | Ala | His | His | Ala | Asp | Ser | Leu | Tyr | Thr | Tyr | Pro | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Thr | Gln | Cys | His | Cys | Gly | Lys | Cys | Asp | Ser | Asp | Ser | Thr | Asp | Cys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Val | Arg | Gly | Leu | Gly | Pro | Ser | Tyr | Cys | Gly | Ser | Gly | Ser | Gly | Ser |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Ala | Pro | Asp | Val | Gln | Asp | Cys | Pro | Glu | Cys | Thr | Leu | Gln | Glu |
|     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| Asn | Pro | Phe | Phe | Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu | Gln | Cys | Met | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Cys | Cys | Phe | Ser | Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg | Ser | Lys | Lys | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Met | Leu | Val | Gln | Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr | Cys | Cys | Val | Ala |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Lys | Ser | Tyr | Asn | Arg | Val | Thr | Val | Met | Gly | Gly | Phe | Lys | Val | Glu | Asn |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| His | Thr | Ala | Cys | His | Cys | Ser | Thr | Cys | Tyr | Tyr | His | Lys | Ser |     |     |
| 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs

87

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTACCTTAA | GATTTGTGAT | AATAACAAGT | ACTGCAGTGG | CACGCCGTGT | GGTTCTCCAC | 60  |
| TTTGAAACCC | CCCATTACTG | TGACCCTGTT | ATATGATTTA | GCTACACAGC | AAGTGGACTC | 120 |
| TGAGGTGACG | TTCTTTTGGG | CCAACATCGT | CTTCTTGGAC | CTTAGTGGAG | TGGGATATGC | 180 |
| TCTAGAGAAG | CAGCAGCCCA | TGCACTGAAG | TATTGGGGCA | CCCGGCTGGG | AGAAGAATGG | 240 |
| GTTTTCTGT  | AGCGTGCATT | CTGGGCAATC | CTGCACATCA | GGAGCGCTAC | CAGATCCGCT | 300 |
| ACCGGATCCG | CAGTAGCTGG | GCCCCAGGCC | TCGCACAGTA | CAATCAGTGC | TGTCGCTGTC | 360 |
| ACACTTGCCA | CAGTGACACT | GGGTGGCCAC | TGGGTATGTA | TACAAGGAAT | CTGCATGGTG | 420 |
| AGCACAGCCG | GGCACTCTCA | CTGTTTCATA | TACCAGTTCC | TTGAAGGTAC | ATGTTTTCTG | 480 |
| GATTTTGGGC | CTGGCTGGGT | CCTTATACAC | CAGATCCCTG | GTGTAGCAGT | AGCCAGCACA | 540 |
| CCAAGTGGTG | TTGATGCTTA | TGCAGAAACG | ACATTCTTCT | TTCTCTATTG | CAATGGTGAT | 600 |
| GTTGGTCAGC | TCACAGCTAT | TGCAGCAGAT | TGCTTTCCAG | CAACAGAAAA | GGAAGAAAAA | 660 |
| CTGGAGTGTC | TTCATCCTTG | G          |            |            |            | 681 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...303
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGC | GGA | TCC | GGT | AGC | GGA | TCT | GGT | AGC | GCT | CCT | GAT | GTG | CAG | GAT | TGC | 48  |
| Cys | Gly | Ser | Gly | Ser | Gly | Ser | Gly | Ser | Ala | Pro | Asp | Val | Gln | Asp | Cys |     |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CCA | GAA | TGC | ACG | CTA | CAG | GAA | AAC | CCA | TTC | TTC | TCC | CAG | CCG | GGT | GCC | 96  |
| Pro | Glu | Cys | Thr | Leu | Gln | Glu | Asn | Pro | Phe | Phe | Ser | Gln | Pro | Gly | Ala |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CCA | ATA | CTT | CAG | TGC | ATG | GGC | TGC | TGC | TTC | TCT | AGA | GCA | TAT | CCC | ACT | 144 |
| Pro | Ile | Leu | Gln | Cys | Met | Gly | Cys | Cys | Phe | Ser | Arg | Ala | Tyr | Pro | Thr |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| CCA | CTA | AGG | TCC | AAG | AAG | ACG | ATG | TTG | GTC | CAA | AAG | CAA | GTC | ACC | TCA | 192 |
| Pro | Leu | Arg | Ser | Lys | Lys | Thr | Met | Leu | Val | Gln | Lys | Gln | Val | Thr | Ser |     |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| GAG | TCC | ACT | TGC | TGT | GTA | GCT | AAA | TCA | TAT | AAC | AGG | GTC | ACA | GTA | ATG | 240 |
| Glu | Ser | Thr | Cys | Cys | Val | Ala | Lys | Ser | Tyr | Asn | Arg | Val | Thr | Val | Met |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| GGG | GGT | TTC | AAA | GTG | GAG | CAA | CAC | ACG | GCG | TGC | CAC | TGC | AGT | ACT | TGT | 288 |

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Gly Gly Phe Lys Val Glu Gln His Thr Ala Cys His Cys Ser Thr Cys  
85 90 95

TAT TAT CAC AAA TCT TAAGGTACC  
Tyr Tyr His Lys Ser  
100

312

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Cys Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys  
1 5 10 15  
Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala  
20 25 30  
Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr  
35 40 45  
Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Gln Val Thr Ser  
50 55 60  
Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
65 70 75 80  
Gly Gly Phe Lys Val Glu Gln His Thr Ala Cys His Cys Ser Thr Cys  
85 90 95  
Tyr Tyr His Lys Ser  
100

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTACCGGTAC CTTAAGATTT GTGATAATAA CAAGTACTGC AGTGGCACGC CGTGTGTTGC 60  
TCCACTTTGA AACCCCCCAT TACTGTGACC CTGTTATATG ATTTAGCTAC ACAGCAAGTG 120  
GACTCTGAGG TGAATTGCTT TTGGACCAAC ATCGTCTTCT TGGACCTTAG TGGAGTGGGA 180  
TATGCTCTAG AGAAGCAGCA GCCCATGCAC TGAAGTATTG GGGCACCCGG CTGGGAGAAG 240  
AATGGGTTTT CTGTAGCGT GCATTCTGGG CAATCCTGCA CATCAGGAGC GCTACCAGAT 300  
CCGCTACCGG ATCCGCA 317

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

89

(A) LENGTH: 575 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 33...575  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|   |                             |    |
|---|-----------------------------|----|
| ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG                             | ATG GAG ATG TTC CAG GGG CTG | 53 |
|   | Met Glu Met Phe Gln Gly Leu |    |
|   | 1 5                         |    |
| CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG | 101                         |    |
| Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu |                             |    |
| 10 15 20  |                             |    |
| CCG CTT CGG CCA CGG TGC CGC CCC ATC CAA GCC ACC CTG GCT GTG GAG | 149                         |    |
| Pro Leu Arg Pro Arg Cys Arg Pro Ile Gln Ala Thr Leu Ala Val Glu |                             |    |
| 25 30 35  |                             |    |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 197                         |    |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala |                             |    |
| 40 45 50 55   |                             |    |
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC | 245                         |    |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala |                             |    |
| 60 65 70  |                             |    |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC | 293                         |    |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile |                             |    |
| 75 80 85  |                             |    |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC | 341                         |    |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala |                             |    |
| 90 95 100   |                             |    |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC | 389                         |    |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp |                             |    |
| 105 110 115   |                             |    |
| TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC | 437                         |    |
| Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe |                             |    |
| 120 125 130 135   |                             |    |
| CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA | 485                         |    |
| Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro |                             |    |
| 140 145 150   |                             |    |
| TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC | 533                         |    |
| Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser |                             |    |
| 155 160 165   |                             |    |

GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA  
 Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro  
 170 175 180

575

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Phe | Gln | Gly | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Met | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Thr | Trp | Ala | Ser | Lys | Glu | Pro | Leu | Arg | Pro | Arg | Cys | Arg | Pro | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ala | Thr | Leu | Ala | Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asn | Thr | Thr | Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gln | Gly | Val | Leu | Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Arg | Phe | Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Pro | Val | Val | Ser | Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Arg | Arg | Ser | Thr | Thr | Asp | Cys | Gly | Gly | Pro | Lys | Asp | His | Pro | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Cys | Asp | Asp | Pro | Arg | Phe | Gln | Asp | Ser | Ser | Ser | Ser | Lys | Ala | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Pro | Ser | Leu | Pro | Ser | Pro | Ser | Arg | Leu | Pro | Gly | Pro | Ser | Asp | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Pro | Ile | Leu | Pro | Gln | Gly | Ser | Gly | Ser | Gly | Ser | Gly | Ser | Ala | Pro | Asp |
|     |     |     |     | 165 |     |     | 170 |     |     |     |     |     |     | 175 |     |
| Val | Gln | Asp | Cys | Pro |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TGGGCAATCC | TGCACATCAG | GAGCGCTACC | AGATCCGCTA | CCGGATCCTT | GGGGGAGGAT | 60  |
| CGGGGTGTCC | GAGGGCCCCG | GGAGTCGGGA | TGGGCTTGGA | AGGCTGGGGG | GAGGGGCCTT | 120 |
| TGAGGAAGAG | GAGTCCTGGA | AGCGGGGGTC | ATCACAGGTC | AAGGGGTGGT | CCTTGGGACC | 180 |

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| CCCCGAGTCA  | GTGGTGCTGC | GGCGGCAGAG | TGCACATTGA | CAGCTGAGAG | CCACGGCGTA | 240 |
| GGAGACCACG  | GGGTTCACGC | CGCGCGGGCA | GCCAGGGAGC | CGGATGGACT | CGAAGCGCAC | 300 |
| ATCGCGGTAG  | TTGCACACCA | CCTGAGGCAG | GGCCGGCAGG | ACCCCTGCA  | GCACGCGGGT | 360 |
| CATGGTGGGG  | CAGTAGCCGG | CACAGATGGT | GGTGTGACG  | GTGATGCACA | CGGGGCAGCC | 420 |
| CTCCTTCTCC  | ACAGCCAGGG | TGGCTTGGAT | GGGGCGGCAC | CGTGGCCGAA | GCGGCTCCTT | 480 |
| GGATGCCCCAT | GTCCCCGCCA | TGCTCAGCAG | CAGCAACAGC | AGCAGCCCCT | GGAACATCTC | 540 |
| CATCCTTGG   |            |            |            |            |            | 549 |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...827
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATGAAATCGA | CGGAATCAGA | CTCGAGCCAA | GG  | ATG | GAG | ATG | TTC | CAG | GGG | CTG | 53  |     |     |     |     |     |
|            |            |            |     | Met | Glu | Met | Phe | Gln | Gly | Leu |     |     |     |     |     |     |
|            |            |            |     | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |
| CTG        | CTG        | TTG        | CTG | CTG | CTG | AGC | ATG | GGC | GGG | ACA | TGG | GCA | TCC | AAG | GAG | 101 |
| Leu        | Leu        | Leu        | Leu | Leu | Leu | Ser | Met | Gly | Gly | Thr | Trp | Ala | Ser | Lys | Glu |     |
|            |            | 10         |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     |
| CCG        | CTT        | CGG        | CCA | CGG | TGC | CGC | CCC | ATC | AAT | GCC | ACC | CTG | GCT | GTG | GAG | 149 |
| Pro        | Leu        | Arg        | Pro | Arg | Cys | Arg | Pro | Ile | Asn | Ala | Thr | Leu | Ala | Val | Glu |     |
|            |            | 25         |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     |     |
| AAG        | GAG        | GGC        | TGC | CCC | GTG | TGC | ATC | ACC | GTC | AAC | ACC | ACC | ATC | TGT | GCC | 197 |
| Lys        | Glu        | Gly        | Cys | Pro | Val | Cys | Ile | Thr | Val | Asn | Thr | Thr | Ile | Cys | Ala |     |
| 40         |            |            |     |     | 45  |     |     |     | 50  |     |     |     |     |     | 55  |     |
| GGC        | TAC        | TGC        | CCC | ACC | ATG | ACC | CGC | GTG | CTG | CAG | GGG | GTC | CTG | CCG | GCC | 245 |
| Gly        | Tyr        | Cys        | Pro | Thr | Met | Thr | Arg | Val | Leu | Gln | Gly | Val | Leu | Pro | Ala |     |
|            |            |            |     | 60  |     |     |     | 65  |     |     |     |     | 70  |     |     |     |
| CTG        | CCT        | CAG        | GTG | GTG | TGC | AAC | TAC | CGC | GAT | GTG | CGC | TTC | GAG | TCC | ATC | 293 |
| Leu        | Pro        | Gln        | Val | Val | Cys | Asn | Tyr | Arg | Asp | Val | Arg | Phe | Glu | Ser | Ile |     |
|            |            |            | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |
| CGG        | CTC        | CCT        | GGC | TGC | CCG | CGC | GGC | GTG | AAC | CCC | GTG | GTC | TCC | TAC | GCC | 341 |
| Arg        | Leu        | Pro        | Gly | Cys | Pro | Arg | Gly | Val | Asn | Pro | Val | Val | Ser | Tyr | Ala |     |
|            |            | 90         |     |     |     |     | 95  |     |     |     | 100 |     |     |     |     |     |
| GTG        | GCT        | CTC        | AGC | TGT | CAA | TGT | GCA | CTC | TGC | CGC | CGC | AGC | ACC | ACT | GAC | 389 |
| Val        | Ala        | Leu        | Ser | Cys | Gln | Cys | Ala | Leu | Cys | Arg | Arg | Ser | Thr | Thr | Asp |     |
|            |            | 105        |     |     |     | 110 |     |     |     | 115 |     |     |     |     |     |     |
| TGC        | GGG        | GGT        | CCC | AAG | GAC | CAC | CCC | TTG | ACC | TGT | GAT | GAC | CCC | CGC | TTC | 437 |

|   |     |
|---|-----|
| Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe |     |
| 120 125 130 135   |     |
| CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA | 485 |
| Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro |     |
| 140 145 150   |     |
| TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC | 533 |
| Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser |     |
| 155 160 165   |     |
| GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA TGC | 581 |
| Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys |     |
| 170 175 180   |     |
| ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA CTT | 629 |
| Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu |     |
| 185 190 195   |     |
| CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA AGG | 677 |
| Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg |     |
| 200 205 210 215   |     |
| TCC AAG AAG ACG ATG TTG GTC CAA AAG CAA GTC ACC TCA GAG TCC ACT | 725 |
| Ser Lys Lys Thr Met Leu Val Gln Lys Gln Val Thr Ser Glu Ser Thr |     |
| 220 225 230   |     |
| TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT TTC | 773 |
| Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe |     |
| 235 240 245   |     |
| AAA GTG GAG CAA CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT CAC | 821 |
| Lys Val Glu Gln His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His |     |
| 250 255 260   |     |
| AAA TCT TAAGTTAACC  | 837 |
| Lys Ser   |     |
| 265   |     |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|   |  |
|---|--|
| Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly     |  |
| 1 5 10 15   |  |
| Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile |  |
| 20 25 30  |  |

93

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr  
 35 40 45  
 Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val  
 50 55 60  
 Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg  
 65 70 75 80  
 Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val  
 85 90 95  
 Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu  
 100 105 110  
 Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu  
 115 120 125  
 Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Lys Ala Pro  
 130 135 140  
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr  
 145 150 155 160  
 Pro Ile Leu Pro Gln Gly Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp  
 165 170 175  
 Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser  
 180 185 190  
 Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg  
 195 200 205  
 Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys  
 210 215 220  
 Gln Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg  
 225 230 235 240  
 Val Thr Val Met Gly Gly Phe Lys Val Glu Gln His Thr Ala Cys His  
 245 250 255  
 Cys Ser Thr Cys Tyr Tyr His Lys Ser  
 260 265

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| TCCGGATTAG | CTTGAGATGG | ATCCGGTTAA | CTTAAGATTT  | GTGATAATAA | CAAGTACTGC | 60  |
| AGTGGCACGC | CGTGTGTTGC | TCCACTTTGA | AACCCCCCAT  | TACTGTGACC | CTGTTATATG | 120 |
| ATTTAGCTAC | ACAGCAAGTG | GACTCTGAGG | TGACTTGCTT  | TTGGACCAAC | ATCGTCTTCT | 180 |
| TGGACCTTAG | TGGAGTGGGA | TATGCTCTAG | AGAAGCAGCA  | GCCCATGCAC | TGAAGTATTG | 240 |
| GGGCACCCGG | CTGGGAGAAG | AATGGGTTTT | CCTGTAGCGT  | GCATTCTGGG | CAATCCTGCA | 300 |
| CATCAGGAGC | GCTACCAGAT | CCGCTACCGG | ATCCTTGGGG  | GAGGATCGGG | GTGTCCGAGG | 360 |
| GCCCCGGGAG | TCGGGATGGG | CTTGGAAGGC | TGGGGGGAGG  | GGCCTTTGAG | GAAGAGGAGT | 420 |
| CCTGGAAGCG | GGGGTCATCA | CAGGTCAAGG | GGTGGTCCTT  | GGGACCCCCG | CAGTCAGTGG | 480 |
| TGCTGCGGCG | GCAGAGTGCA | CATTGACAGC | TGAGAGCCAC  | GGCGTAGGAG | ACCACGGGGT | 540 |
| TCACGCCGCG | CGGGCAGCCA | GGGAGCCGGA | TGGACTCGAA  | GCGCACATCG | CGGTAGTTGC | 600 |
| ACACCACCTG | AGGCAGGGCC | GGCAGGAGCC | CCTGCAGCAC  | GCGGGTCATG | GTGGGGCAGT | 660 |
| AGCCGGCACA | GATGGTGGTG | TTGACGGTGA | TGCACACGGG  | GCAGCCCTCC | TTCTCCACAG | 720 |
| CCAGGGTGGC | ATTGATGGGG | CGGCACCGTG | GCCGAAGCGG  | CTCCTTGGAT | GCCCATGTCC | 780 |
| CGCCCATGCT | CAGCAGCAGC | AACAGCAGCA | GCCCCCTGGAA | CATCTCCATC | CTTGG      | 835 |

94

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGAGGAAGGG TGGTCGACCT CTCTGGT

27

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACATCAGGA GCTTGTGGGA GGATCGG

27

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATCCTCCCAC AAGCTCCTGA TGTGCAG

27

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGAGTCGACA TGATAATTCA GTGATTGAAT

30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGATGGAGAT GTTCCAGGGG CTGCT 55

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCTACCAGAT CCGCTACCGG ATCCTTGGGG GAGGATCGGG GTGTCCGAGG G 51

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGATCCGGTA GCGGATCTGG TAGCGCTCCT GATGTGCAGG ATTGCCCA 48

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCCGGATTAG CTTGAGATGG ATCCGGTACC TTAAGATTTG TGATAATAAC AAGTACTGCA 60

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG

32

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCCGGATTAG CTTGAGATGG ATCCGGTACC TTA

33

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Phe | Gln | Gly | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Met | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Thr | Trp | Ala |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Gly | Ser | Gly | Ser | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

97

GCTACCGGAT CCCC GCGGGT CATCACAGGT CAAGGGGTGG T

41

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGAATGGAGA TGCTCCAGGG GCTGCT

56

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCTACCAGAT CCGCTACCGG ATCCTTGGGG GTGGTCACAG GTCAAGGGGT G

51

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Met | Leu | Gln | Gly | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Met | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Trp | Ala |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGATGAAGAC ACTCCAGTTT TTCTTCC

57

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACCAGATCCG CTACCGGATC CTTCTTTCAT TTCACCAAAG GAGCAG

46

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile  
1 5 10 15  
Cys Cys

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GCTACCGGAT CCTTCTTTCA TTTCACCAA GGAGCAGTAG CTGGGCCCCA GGCCTCGCAC 60  
AGTACAATCA GTGCTGTCGC TGTCGCAGAG TGCACATTGA CAGCTGACAG C 111

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCTACCGGAT CCTTCTTTCA TTTCACCAA GGAGCAGTAG CTGGGCCCCA GGCCTCGCAC 60  
AGTGCAATCA GTGGTGCTGC GCGCGCA 87

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|   |    |
|---|----|
| GCTACCGGAT CCTTCACCAA AGGAGCAGTA GCTGGGCCCC AGGCCTCGCA CAGTGCACTC | 60 |
| AGTGGTGCTG CGGCGGCA   | 78 |

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|   |    |
|---|----|
| GCTACCGGAT CCCCGCGGGT CATCGCAGTA GCTGGGCCCC AGGCCTCGCA CAGTGCACTC | 60 |
| AGTGGTGCTG CGGCGGCA   | 78 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

|   |    |
|---|----|
| TGCTTCTCTA GAGCATATCC CACTCCACTA AGGTCCAAGA AGACGATGTT GGTCCAAAAG | 60 |
| CAAGTCACCT  | 70 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|   |    |
|---|----|
| GTACCGGTAC CTTAAGATTT GTGATAATAA CAAGTACTGC AGTGGCACGC CGTGTGTTGC | 60 |
| TCCACTTTGA AAC  | 73 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CGGGGTAGGT TCGGTGGGAC CGACACCTCT TCCTCCCGAC GGGG

44

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTACCACCAC AACTGCCACT ACGTGTGCCC CGTCGGGAGG AAGAGGTG

48

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Lys | Glu | Pro | Leu | Arg | Pro | Arg | Cys | Arg | Pro | Ile | Asn | Ala | Thr | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr | Val | Asn | Thr | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg | Val | Leu | Gln | Gly | Val |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr | Arg | Asp | Val | Arg | Phe |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val | Asn | Pro | Val | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ser | Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala | Leu | Cys | Arg | Arg | Ser |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Thr | Thr | Asp | Cys | Gly | Gly | Pro | Lys | Asp | His | Pro | Leu | Thr | Cys | Asp | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Arg | Phe | Gln | Asp | Ser | Ser | Ser | Ser | Lys | Ala | Pro | Pro | Pro | Ser | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Pro | Ser | Pro | Ser | Arg | Leu | Pro | Gly | Pro | Ser | Asp | Thr | Pro | Ile | Leu | Pro |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Glu | Pro | Leu | Arg | Pro | Arg | Cys | Arg | Pro | Ile | Asn | Ala | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr | Val | Asn | Thr | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg | Val | Leu | Gln | Gly | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr | Arg | Asp | Val | Arg | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val | Asn | Pro | Val | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala | Leu | Cys | Arg | Arg | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Thr | Asp | Cys | Gly | Gly | Pro | Lys | Asp | His | Pro | Leu | Thr | Cys | Asp | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Glu | Pro | Leu | Arg | Pro | Arg | Cys | Arg | Pro | Ile | Asn | Ala | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr | Val | Asn | Thr | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg | Val | Leu | Gln | Gly | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr | Arg | Asp | Val | Arg | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val | Asn | Pro | Val | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala | Leu | Cys |     |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Glu | Pro | Leu | Arg | Pro | Trp | Cys | His | Pro | Ile | Asn | Ala | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr | Val | Asn | Thr | Thr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Met | Arg | Val | Leu | Gln | Ala | Val |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Pro | Pro | Leu | Pro | Gln | Val | Val | Cys | Thr | Tyr | Arg | Asp | Val | Arg | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Glu | Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val | Asp | Pro | Val | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Phe | Pro | Val | Ala | Leu | Ser | Cys | Arg | Cys | Gly | Pro | Cys | Arg | Arg | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Ser | Asp | Cys | Gly | Gly | Pro | Lys | Asp | His | Pro | Leu | Thr | Cys | Asp | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Pro | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Cys | Glu | Leu | Thr | Asn | Ile | Thr | Ile | Ala | Val | Glu | Lys | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Cys | Gly | Phe | Cys | Ile | Thr | Ile | Asn | Thr | Thr | Trp | Cys | Ala | Gly | Tyr | Cys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Tyr | Thr | Arg | Asp | Leu | Val | Tyr | Lys | Asp | Pro | Ala | Arg | Pro | Lys | Ile | Gln |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Thr | Cys | Thr | Phe | Lys | Glu | Leu | Val | Tyr | Glu | Thr | Val | Arg | Val | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Cys | Ala | His | His | Ala | Asp | Ser | Leu | Tyr | Thr | Tyr | Pro | Val | Ala | Thr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Gln | Cys | His | Cys | Gly | Lys | Cys | Asp | Ser | Asp | Ser | Thr | Asp | Cys | Thr | Val |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Arg | Gly | Leu | Gly | Pro | Ser | Tyr | Cys | Ser | Phe | Gly | Glu | Met | Lys | Glu |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Cys | Glu | Leu | Thr | Asn | Ile | Thr | Ile | Ala | Val | Glu | Lys | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Gly | Phe | Cys | Ile | Thr | Ile | Asn | Thr | Thr | Trp | Cys | Ala | Gly | Tyr | Cys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Tyr | Thr | Arg | Asp | Leu | Val | Tyr | Lys | Asp | Pro | Ala | Arg | Pro | Lys | Ile | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Thr | Cys | Thr | Phe | Lys | Glu | Leu | Val | Tyr | Glu | Thr | Val | Arg | Val | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Cys | Ala | His | His | Ala | Asp | Ser | Leu | Tyr | Thr | Tyr | Pro | Val | Ala | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Cys | His | Cys | Gly | Lys | Cys | Asp | Ser | Asp | Ser | Thr | Asp | Cys | Thr | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Gly | Leu | Gly | Pro | Ser | Tyr | Cys | Ser | Phe | Gly | Glu |     |     |     |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Cys | Glu | Leu | Thr | Asn | Ile | Thr | Ile | Ala | Val | Glu | Lys | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Gly | Phe | Cys | Ile | Thr | Ile | Asn | Thr | Thr | Trp | Cys | Ala | Gly | Tyr | Cys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Tyr | Thr | Arg | Asp | Leu | Val | Tyr | Lys | Asp | Pro | Ala | Arg | Pro | Lys | Ile | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Thr | Cys | Thr | Phe | Lys | Glu | Leu | Val | Tyr | Glu | Thr | Val | Arg | Val | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Cys | Ala | His | His | Ala | Asp | Ser | Leu | Tyr | Thr | Tyr | Pro | Val | Ala | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Cys | His | Cys | Gly | Lys | Cys | Asp | Ser | Asp | Ser | Thr | Asp | Cys | Thr | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Gly | Leu | Gly | Pro | Ser | Tyr | Cys |     |     |     |     |     |     |     |     |
|     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Asp | Ser | Thr | Asp | Cys | Thr | Val | Arg | Gly | Leu | Gly | Pro | Ser | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

104

Cys Ser Phe Gly Glu Met Lys Glu  
20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys  
1 5 10 15  
Glu

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Thr Val Arg Gly Leu Gly Pro Ser Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Asp | Val | Gln | Asp | Cys | Pro | Glu | Cys | Thr | Leu | Gln | Glu | Asn | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Phe | Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu | Gln | Cys | Met | Gly | Cys | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg | Ser | Lys | Lys | Thr | Met | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gln | Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr | Cys | Cys | Val | Ala | Lys | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Asn | Arg | Val | Thr | Val | Met | Gly | Gly | Phe | Lys | Val | Glu | Asn | His | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Cys | His | Cys | Ser | Thr | Cys | Tyr | Tyr | His | Lys | Ser |     |     |     |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gly Ser Gly Ser  
1

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Ser Gly Ser Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

1026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Asp Asp Pro Arg

1

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